



ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF  
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**FIGURE 23**

**Figure 23A**

Section 1					
	(1)	10	20	30	40 51
CUR2-1.6.1_HC	(1)	EVQLVESGGGLVQPKGGSLRLSCAASGFER			
VH3-21	(1)	EVQLVESGGGLVQPKGGSLRLSCAASGFTES			
Consensus	(1)	EVQLVESGGGLVQPKGGSLRLSCAASGF F SY MNWVROAPGRGLEWVSSI			
Section 2					
	(52)	60	70	80	90 102
CUR2-1.6.1_HC	(52)	SSSSSNLYADSVKGRFTISRDNAKNSLYLQMN			
VH3-21	(52)	SSSSSVLYADSVKGRFTISRDNAKNSLYLQMN			
Consensus	(52)	SSSSS IYYADSVKGRFTISRDNAKNSLYLQMN			
Section 3					
	(103)	110	126		
CUR2-1.6.1_HC	(103)	TFGGIIASFYFDYWGQGLTVTVSS			
VH3-21	(99)	-----			
Consensus (103)					

**Figure 23B**

Section 1					
	(1)	10	20	30	40 51
CUR2-1.6.1 LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI			
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI			
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI			
Section 2					
	(52)	60	70	80	90 102
CUR2-1.6.1 LC	(52)	SSIQSGVPSRFSGSGSGTEFTLTIS			
A30	(52)	SSIQSGVPSRFSGSGSGTEFTLTIS			
Consensus	(52)	SSIQSGVPSRFSGSGSGTEFTLTIS			
Section 3					
	(103)	103	107		
CUR2-1.6.1 LC	(103)	KVEIK			
A30	(96)	-----			
Consensus	(103)				



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**FIGURE 24**

**Figure 24A**

		Section 1						
		(1)	1	10	20	30	40	51
Cur2-1.11.1 HC	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						
VH3-53	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						
Consensus	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						
		Section 2						
		(52)	52	60	70	80	90	102
Cur2-1.11.1 HC	(52)	YSGGSTYYADSVKGRFTISRDNISKNTLYLQMSLPAEDTAVYYCAGTVTTN						
VH3-53	(52)	YSGGSTYYADSVKGRFTISRDNISKNTLYLQMSLPAEDTAVYYCAR-----						
Consensus	(52)	YSGGSTYYADSVKGRFTISRDNISKNTLYLQMSLPAEDTAVYYCA						
		Section 3						
		(103)	103	110	120			
Cur2-1.11.1 HC	(103)	YYYGMDVWGQGTITVTVSS				SEQ ID NO:15		
VH3-53	(98)	-----				SEQ ID NO:5		
Consensus	(103)							

**Figure 24B**

Section 1						
	(1)	1	10	20	30	40 51
CUR2-1.11.1 LC	(1)	DIIVMTQSPLSLPVTPGEPASISCRSSQSLHNGYNYLDWYLQKPGQSPQQL				
A19	(1)	DIIVMTQSPLSLPVTPGEPASISCRSSQSLHNGYNYLDWYLQKPGQSPQQL				
Consensus	(1)	DIIVMTQSPLSLPVTPGEPASISCRSSQSLHNGYNYLDWYLQKPGQSPQQL				
Section 2						
	(52)	52	60	70	80	90 102
CUR2-1.11.1 LC	(52)	LIYLGSNRAAGVPRDFSGSGSGTDFTLKISRVEAEDVGVVYCMQALQTLP				
A19	(52)	LIYLGSNRAAGVPRDFSGSGSGTDFTLKISRVEAEDVGVVYCMQALQTF--				
Consensus	(52)	LIYLGSNRAAGVPRDFSGSGSGTDFTLKISRVEAEDVGVVYCMQALQT				
Section 3						
	(103)	103	111			
CUR2-1.11.1 LC	(103)	GGGTRVEIK		SEQ ID NO:16		
A19	(101)	-----		SEQ ID NO:8		
Consensus	(103)					





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**FIGURE 26**

**Figure 26A**

								Section 1
	(1)	1	10	20	30	40	52	
CR2-1.18_HC	(1)	QVQLVQSGAEVVKRPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN						
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN						
Consensus	(1)	QVQLVQSGAEVVKRPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN						
								Section 2
	(53)	53	60	70	80	90	104	
CR2-1.18_HC	(53)	PNSGNTGYAQRFGQGRVTMTNRTSISTAYMELSSLRSEDVAVYYCAPEGIAVA						
VH1-8	(53)	PNSGNTGYAQRFGQGRVTMTNRTSISTAYMELSSLRSEDVAVYYCAR-----						
Consensus	(53)	PNSGNTGYAQRFGQGRVTMTNRTSISTAYMELSSLRSEDVAVYYCAR						
								Section 3
	(105)	105	110	126				
CR2-1.18_HC	(105)	GTYYYYYGMDVWGQGTITVTVSS			SEQ ID NO:19			
VH1-8	(99)	-----			SEQ ID NO:1			
Consensus	(105)							

**Figure 26B**

								Section 1	
	(1)	1	10	20	30	40	53		
CR2-1.18_LC	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAASS							
A30	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAASS							
Consensus	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAASS							Section 2
	(54)	54	60	70	80	90	106		
CR2-1.18_LC	(54)	LQSGVPSRFP SGSGSGTEFTLTISSLQPEDPATYFCLQHNSYPFTPGPGTKVDI							
A30	(54)	LQSGVPSRFP SGSGSGTEFTLTISSLQPEDPATYFCLQHNSYP-----							
Consensus	(54)	LQSGVPSRFP SGSGSGTEFTLTISSLQPEDPATYFCLQHNSYP							Section 3
	(107)	107							
CR2-1.18_LC	(107)	K	SEQ ID NO:20						
A30	(96)	-	SEQ ID NO:11						
Consensus	(107)								



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**FIGURE 27**

**Figure 27A**

Section 1									
(1)	1	10	20	30	40	50	60	70	80
Cur2-1.19.1_hc	(1)	QVQLVQSGAEVRRKPGASVKVSCPA	SGYTFTHYDINWVRQATGGGLEWMGWMN						
VH1-8	(1)	QVQLVQSGAEVRRKPGASVKVSCPA	SGYTFTHYDINWVRQATGGGLEWMGWMN						
Consensus	(1)	QVQLVQSGAEVRRKPGASVKVSCPA	SGYTFTHYDINWVRQATGGGLEWMGWMN						
Section 2									
(53)	53	60	70	80	90	100	110	120	130
Cur2-1.19.1_hc	(53)	PNSGNTGYAQRFGGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITF							
VH1-8	(53)	PNSGNTGYAQRFGGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----							
Consensus	(53)	PNSGNTGYAQRFGGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR							
Section 3									
(105)	105	110	120	130	140	150	160	170	180
Cur2-1.19.1_hc	(105)	GGVIVHYGMDVWGQGTITVTVSS							
VH1-8	(99)	-----							
Consensus	(105)	GGVIVHYGMDVWGQGTITVTVSS							

**Figure 27B**

Section 1									
(1)	1	10	20	30	40	50	60	70	80
Cur2-1.19.1_lc	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI	RNDLGWYQKPKGAPKRLIYAAAS						
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI	RNDLGWYQKPKGAPKRLIYAAAS						
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI	RNDLGWYQKPKGAPKRLIYAAAS						
Section 2									
(53)	53	60	70	80	90	100	110	120	130
Cur2-1.19.1_lc	(53)	SLQSGVPSRPFGSGSGTFTLTIS	SLOPEDPATYYCLOHNSDFCSFGQGTKL						
A30	(53)	SLQSGVPSRPFGSGSGTFTLTIS	SLOPEDPATYYCLOHNSDFCSFGQGTKL						
Consensus	(53)	SLQSGVPSRPFGSGSGTFTLTIS	SLOPEDPATYYCLOHNSDFCSFGQGTKL						
Section 3									
(105)	105	110	120	130	140	150	160	170	180
Cur2-1.19.1_lc	(105)	EIR							
A30	(96)	---							
Consensus	(105)	EIR							



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FIGURE 28

Figure 28A

		Section 1					
		(1)	1	10	20	30	40 51
Cur2-1.23.1_HC	(1)	EVQLVQSGAEVKKPGEGLKRIISCEGSGYSPFTTHYWGIVRQMPGKGLWWMGII					
VH5-51	(1)	EVQLVQSGAEVKKPGEGLKISCKGSGYSPFTSYWIGVRAQMPGKGLWWMGII					
Consensus	(1)	EVQLVQSGAEVKKPGEGLKISCGSGYSPFTSYWIGVRAQMPGKGLWWMGII					
		Section 2					
		(52)	52	60	70	80	90 102
Cur2-1.23.1_HC	(52)	YPGDSDTTRYSPFQGGVTISADKSIISTAYLQWSSLKASDTAMYYCARHVS					
VH5-51	(52)	YPGDSDTTRYSPFQGGVTISADKSIISTAYLQWSSLKASDTAMYYCAR----					
Consensus	(52)	YPGDSDTTRYSPFQGGVTISADKSIISTAYLQWSSLKASDTAMYYCAR					
		Section 3					
		(103)	103	110	126		
Cur2-1.23.1_HC	(103)	YYVSGSYYNVFDYWGQGLVTVSS				SEQ ID NO:23	
VH5-51	(99)	-----				SEQ ID NO:6	
Consensus	(103)						

Figure 28B

										Section 1	
		(1)	1	10	20	30	40	51			
Cur2-1.23.1_LC	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISIRNDLGWYQQIPGKAPKRLIYAA									
A30	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISIRNDLGWYQQKPGKAPKRLIYAA									
Consensus	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISIRNDLGWYQQPGKAPKRLIYAA									
										Section 2	
		(52)	52	60	70	80	90	102			
Cur2-1.23.1_LC	(52)	SSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGGT									
A30	(52)	SSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYP-----									
Consensus	(52)	SSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNSYP									
										Section 3	
		(103)	103	107							
Cur2-1.23.1_LC	(103)	KVEIK	SEQ ID NO:24								
A30	(96)	-----	SEQ ID NO:11								
Consensus	(103)										



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**FIGURE 29**

**Figure 29A**

		Section 1					
		(1)	1	10	20	30	40 51
CR2-1.24.1 HC	(1)	QVQLVESGGGVVQPGGSLRLSCAASGFPSSYGMHWVROAPGKGLEWVADI					
VH3-33	(1)	QVQLVESGGGVVQPGGSLRLSCAASGFPSSYGMHWVROAPGKGLEWVAVI					
Consensus	(1)	QVQLVESGGGVVQPGGSLRLSCAASGFPSSYGMHWVROAPGKGLEWVA I					
		Section 2					
		(52)	52	60	70	80	90 102
CR2-1.24.1 HC	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGY					
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR----					
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR					
		Section 3					
		(103)	103	110	126		
CR2-1.24.1 HC	(103)	SYGYVYDYGMDVWGQGTTVTVSS				SEQ ID NO:25	
VH3-33	(99)	-----				SEQ ID NO:4	
Consensus	(103)						

**Figure 29B**

								Section 1		
		(1)	1	10	20	30	40	52		
CR2-1.24.1 LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAAS								
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAAS								
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQRPGKAPKRLIYAAS								
								Section 2		
		(53)	53	60	70	80	90	104		
CR2-1.24.1 LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYEWTFGQGTKV								
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYP-----								
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYP								
								Section 3		
		(105)	1067							
CR2-1.24.1 LC	(105)	EIK	SEQ ID NO:26							
A30	(96)	---	SEQ ID NO:11							
Consensus	(105)									

		Section 1						
		(1)	10	20	30	40	52	
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASGQIRNDLGWYQOKPGKAPKRLIYAA						
CR2-1.25.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASGQIRNDLGWYQOKPGKAPKRLIYAA						
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASGQIRNDLGWYQOKPGKAPKRLIYAA						
		Section 2						
		(53)	53	60	70	80	90	104
A30	(53)	SLQSGVPRFRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----						
CR2-1.25.1_LC	(53)	SLQSGVPRFRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPRTWTFGGQGTKV						
Consensus	(53)	SLQSGVPRFRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP						
		Section 3						
		(105)	1067					
A30	(96)	---	SEQ ID NO:11					
CR2-1.25.1_LC	(105)	EIK	SEQ ID NO:28					
Consensus	(105)							





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**FIGURE 31**

**Figure 31A**

Section 1									
	(1)	10	20	30	40	50	60	70	80
VH5-51	(1)	EVQLVQSGAEVKKP	GESLKISCKGSGYSFTSYWIGWVR	OMP	PGKGLEWMGI	IIY			
CR2-1.29_HC	(1)	EVQLVQSGAEVKKP	GESLKISCKGSGYSFTSYWIGWVR	OMP	PGKGLEWMGI	IIY			
Consensus	(1)	EVQLVQSGAEVKKP	GESLKISCKGSGYSFTSYWIGWVR	OMP	PGKGLEWMGI	IIY			
Section 2									
	(53)	53	60	70	80	90	100	110	120
VH5-51	(53)	PGDS	TRYSPSP	FGQQT	ISADRS	ISTAYLQWSS	LKASDT	AMYYCAR	-----
CR2-1.29_HC	(53)	PGDS	TRYSPSP	FGQQT	ISADRS	ISTAYLQWSS	LKASDT	AMYYCAR	HVDVGA
Consensus	(53)	PGDS	TRYSPSP	FGQQT	ISADRS	ISTAYLQWSS	LKASDT	AMYYCAR	
Section 3									
	(105)	105	110	120	130	140	150	160	170
VH5-51	(99)	-----	-----	-----	-----	-----	-----	-----	-----
CR2-1.29_HC	(105)	TIGGY	YYYYHGM	DVWGQ	TTVT	VSS			
Consensus	(105)	TIGGY	YYYYHGM	DVWGQ	TTVT	VSS			

**Figure 31B**

Section 1									
	(1)	10	20	30	40	50	60	70	80
A19	(1)	DI	VTQSP	LSLP	VT	PGEP	ASIS	CRSS	SQSLH
CR2-1.29_LC	(1)	DI	VTQSP	LSLP	VT	PGEP	ASIS	CRSS	SQSLH
Consensus	(1)	DI	VTQSP	LSLP	VT	PGEP	ASIS	CRSS	SQSLH
Section 2									
	(54)	54	60	70	80	90	100	110	120
A19	(54)	YLGS	NRAS	GV	PD	RF	SGSG	SGT	DFTLKISR
CR2-1.29_LC	(54)	YLGS	NRAS	GV	PD	RF	SGSG	SGT	DFTLKISR
Consensus	(54)	YLGS	NRAS	GV	PD	RF	SGSG	SGT	DFTLKISR
Section 3									
	(107)	107	113	120	130	140	150	160	170
A19	(101)	-----	-----	-----	-----	-----	-----	-----	-----
CR2-1.29_LC	(107)	G	T	K	L	E	I	K	
Consensus	(107)	G	T	K	L	E	I	K	



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**FIGURE 32**

**Figure 32A**

								Section 1	
	(1)	1	10	20	30	40	52		
VH1-18	(1)	QVQLVQSGAEVRRPGASVKVSCFASGYTFSTSYGTSWVRQAPGGGLEWMGWIS							
CR2-1.33_HC	(1)	QVQLVQSGAEVKKPGASVKVSCFASGYTFSTSYGISWVRQAPGGGLEWMGWIS							
Consensus	(1)	QVQLVQSGAEVRRPGASVKVSCFASGYTFSTSYGISWVRQAPGGGLEWMGWIS							
								Section 2	
	(53)	53	60	70	80	90	104		
VH1-18	(53)	AYNGNTNYACKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----							
CR2-1.33_HC	(53)	AYNGNTNYACKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYIDS							
Consensus	(53)	AYNGNTNYACKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR							
								Section 3	
	(105)	105	110	127					
VH1-18	(99)	-----				SEQ ID NO:2			
CR2-1.33_HC	(105)	SDYLYYYYGLDVWGQGTTVTVSS				SEQ ID NO:31			
Consensus	(105)								

**Figure 32B**

								Section 1
	(1)	1	10	20	30	40	53	
A20	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS						
CR2-1.33_LC	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS						
Consensus	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS						
								Section 2
	(54)	54	60	70	80	90	106	
A20	(54)	LQSGVPSRFSGSGSGTDFTLTITISSLQPEDVATYYCQKYNAP-----						
CR2-1.33_LC	(54)	LQSGVPSRFSGSGSGTDFTLTITISSLQPEDVATYYCQKYNAPLTPGGGTVKVEI						
Consensus	(54)	LQSGVPSRFSGSGSGTDFTLTITISSLQPEDVATYYCQKYNAP						
								Section 3
	(107)	107						
A20	(96)	-					SEQ ID NO:9	
CR2-1.33_LC	(107)	K					SEQ ID NO:32	
Consensus	(107)							



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**FIGURE 33**

**Figure 33A**

								Section 1	
	(1)	1	10	20	30	40	51		
VH3-33	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIT							
CR2-1.38.1_HC	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIT							
Consensus	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAII							
								Section 2	
	(52)	52	60	70	80	90	102		
VH3-33	(52)	WYDGSNRYVADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----							
CR2-1.38.1_HC	(52)	WYDGNDRYYVADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGYYY							
Consensus	(52)	WYDGRYYVADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR							
								Section 3	
	(103)	103	110	127					
VH3-33	(99)	-----				SEQ ID NO:4			
CR2-1.38.1_HC	(103)	DSSDYLYYYYGMDVWGQGTITVTVSS				SEQ ID NO:33			
Consensus	(103)								

**Figure 33B**

								Section 1	
	(1)	1	10	20	30	40	52		
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQKPKGVKLLIYAAS							
CR2-1.38.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQKPKGVNLLIYAAS							
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQKPKGVPLIYAAS							
								Section 2	
	(53)	53	60	70	80	90	104		
A20	(53)	TLQSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKNSAP-----							
CR2-1.38.1_LC	(53)	TLQSGVPSRFSGSGSGTDFTLTISLQPEDVAAYCQKNSAPWTFGQGTIV							
Consensus	(53)	TLQSGVPSRFSGSGSGTDFTLTISLQPEDVA YYCQK NSAP							
								Section 3	
	(105)	1067							
A20	(96)	---	SEQ ID NO:9						
CR2-1.38.1_LC	(105)	EIK	SEQ ID NO:34						
Consensus	(105)								



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### FIGURE 34

Figure 34A

		Section 1				
	(1)	1	10	20	30	40 51
VH5-51	(1)	EVQLVQSGAEVKKPQGGSLKISCKGSGYSPTSYWIGWVRMPGKGLEWMGII				
CR2-1.39.1_HC	(1)	EVQLVQSGTEVKKPQGGSLKISCKGSGYRFTSYWIGWVRMPGKGLEWMGII				
Consensus	(1)	EVQLVQSG EVKKPQGGSLKISCKGSGY FTSYWIGWVRMPGKGLEWMGII				
		Section 2				
	(52)	52	60	70	80	90 102
VH5-51	(52)	YPGDS DTRYSPSFQGGVTLISADKSIISTAYLQWSSLKASDTAMYICAR----				
CR2-1.39.1_HC	(52)	YPGDS DTRYSPSFQGGVTLISADKSIISTAYLQWSSLKASDTAMYICARHGSI				
Consensus	(52)	YPGDS DTRYSPSFQGGVTLISADKSIISTAYLQWSSLKASDTAMYICAR				
		Section 3				
	(103)	103	110	126		
VH5-51	(99)	-----				SEQ ID NO:6
CR2-1.39.1_HC	(103)	YYNSGSIYNVFDYWGQGLVTVSS				SEQ ID NO:35
Consensus	(103)					

Figure 34B

							Section 1
	(1)	1	10	20	30	40	52
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS					
CR2-1.39.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS					
							Section 2
	(53)	53	60	70	80	90	104
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----					
CR2-1.39.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGQGTKV					
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP					
							Section 3
	(105)	1067					
A30	(96)	---	SEQ ID NO:11				
CR2-1.39.1_LC	(105)	EIK	SEQ ID NO:36				
Consensus	(105)						

Section 1						
	(1)	10	20	30	40	53
A20	(1)	DIQMTQSPBSLSASVGDRTITCRASQGISNYLAWYCKQKPGKVPKLLIYAAS				
CR2-1.45_LC	(1)	DIQMTQSPBSLSASVGDRTINCRASQGISNDLAWYQKPGKVPKLLIYAAS				
Consensus	(1)	DIQMTQSPBSLSASVGDRTI CRASQGISN LANYQKPGKVPKLLIYAAS				
Section 2						
	(54)	60	70	80	90	106
A20	(54)	LQSGVPSRFSGSGSGTDFTLTITISLQPEDVATYYCQKYN <del>SAF</del> -----				
CR2-1.45_LC	(54)	LQLGVPSRFSGSGSGTDFTLTITISLQPEDVATYYCQKYN <del>SAF</del> FTFGPGTKVDI				
Consensus	(54)	LQ GVPSPRFSGSGSGTDFTLTITISLQPEDVATYYCQKYN <del>SAF</del>				
Section 3						
	(107)	(107)				
A20	(96)	-	SEQ ID NO:9			
CR2-1.45_LC	(107)	K	SEQ ID NO:39			
Consensus	(107)					



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FIGURE 36

Figure 36A

		Section 1					
		(1)	1	10	20	30	40 51
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVROATGQGLEWMGWM					
CR2-1.46.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVROATGQGLEWMGWM					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVROATGQGLEWMGWM					
		Section 2					
		(52)	52	60	70	80	90 102
VH1-8	(52)	NPNSGNTGYAQKFGGRVTMTNTSISTAYNELSSLRSEDTAIVYYCAR----					
CR2-1.46.1_HC	(52)	NPNNENTGYAQKFGGRVTMTNTSISTAYNELSSLRSEDTAIVYYCARDIVV					
Consensus	(52)	NPN GNTGYAQKFGGRVTMTNTSISTAYNELSSLRSEDTAIVYYCAR					
		Section 3					
		(103)	103	110	126		
VH1-8	(99)	-----				SEQ ID NO:1	
CR2-1.46.1_HC	(103)	VVTATDYYYGMDVWGQGTTVTVSS				SEQ ID NO:40	
Consensus	(103)						

Figure 36B

		Section 1					
		(1)	1	10	20	30	40 52
A30	(1)	DIQMTQSPESLSASVGDRVTITCRASQGIKNDLGWYQKPKGKPKRLITAAAS					
CR2-1.46.1_LC	(1)	DIQMTQSPESLSASVGDRVTITCRASQGIKNDLGWYQKPKGKPKRLITAAAS					
Consensus	(1)	DIQMTQSPESLSASVGDRVTITCRASQGIKNDLGWYQKPKGKPKRLITAAAS					
		Section 2					
		(53)	53	60	70	80	90 104
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----					
CR2-1.46.1_LC	(53)	SLPSSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHSGYPPPTFGQGTKV					
Consensus	(53)	SL SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOH YP					
		Section 3					
		(105)	1057				
A30	(96)	---				SEQ ID NO:11	
CR2-1.46.1_LC	(105)	EIK				SEQ ID NO:41	
Consensus	(105)						



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**FIGURE 37**

**Figure 37A**

		Section 1				
		(1)	1	10	20	30 40 51
CR2-1.48.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKRSGYTFTSYGISWVRQAPGGGLEWMGWI				
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKRSGYTFTSYGISWVRQAPGGGLEWMGWI				
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKRSGYTFTSYGISWVRQAPGGGLEWMGWI				
		Section 2				
		(52)	52	60	70	80 90 102
CR2-1.48.1_HC	(52)	SAYNGNTNYAQRLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCARDVEY				
VH1-18	(52)	SAYNGNTNYAQRLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCAR----				
Consensus	(52)	SAYNGNTNYAQRLQGRVTMTDTSTSTAYMELRSLRSDDTAVYYCAR				
		Section 3				
		(103)	103	110	125	
CR2-1.48.1_HC	(103)	YYDGSGLYYFDYWGQGLVTVSS				SEQ ID NO:42
VH1-18	(99)	-----				SEQ ID NO:2
Consensus	(103)					

**Figure 37B**

		Section 1				
		(1)	1	10	20	30 40 52
CR2-1.48.1_LC	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGISWLAHWYQKPKAPKLLIYAAS				
L5	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGISWLAHWYQKPKAPKLLIYAAS				
Consensus	(1)	DIQMTQSPSSVSASVGDRVTITCRASQGISWLAHWYQKPKAPKLLIYAAS				
		Section 2				
		(53)	53	60	70	80 90 104
CR2-1.48.1_LC	(53)	ILQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCCQNSFPRTFGQGRV				
L5	(53)	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCCQNSFP-----				
Consensus	(53)	LQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCCQANSFP				
		Section 3				
		(105)	1057			
CR2-1.48.1_LC	(105)	EIK				SEQ ID NO:43
L5	(96)	---				SEQ ID NO:7
Consensus	(105)					



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**FIGURE 38**

**Figure 38A**

Section 1								
	(1)	10	20	30	40	51		
CR2-1.49.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTPTSYDINWVRQATGQGLEWMGWM						
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTPTSYDINWVRQATGQGLEWMGWM						
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTPTSYDINWVRQATGQGLEWMGWM						
Section 2								
	(52)	60	70	80	90	102		
CR2-1.49.1_HC	(52)	NPNSGDTGYAQKPGQGRVTMTNTSISTAYMELSSLRSEDTAVYICARMRDI						
VH1-8	(52)	NPNSGNTGYAQKPGQGRVTMTNTSISTAYMELSSLRSEDTAVYICAR----						
Consensus	(52)	NPNSG TGYAQKPGQGRVTMTNTSISTAYMELSSLRSEDTAVYFCAR						
Section 3								
	(103)	103	110	127				
CR2-1.49.1_HC	(103)	VATSYYYYFYGM DVWGQGT TVTVSS			SEQ ID NO:44			
VH1-8	(99)	-----			SEQ ID NO:1			
Consensus	(103)							

**Figure 38B**

Section 1							
	(1)	10	20	30	40	52	
CR2-1.49.1_LC	(1)	DIVMTQSPFLSLPVTPGEPASISCRSSQSLHNSGYNLYDWYLKPGQSPQLL					
A19	(1)	DIVMTQSPFLSLPVTPGEPASISCRSSQSLHNSGYNLYDWYLKPGQSPQLL					
Consensus	(1)	DIVMTQSPFLSLPVTPGEPASISCRSSQSLHNSGYNLYDWYL KPGQSPQLL					
Section 2							
	(53)	53	60	70	80	90	104
CR2-1.49.1_LC	(53)	IYLGSSRASGVDPDRFGSGSGTDFTLKISRVEAEDVGVVYCMQTLQITITFGQ					
A19	(53)	IYLGSSRASGVDPDRFGSGSGTDFTLKISRVEAEDVGVVYCMQALQTP----					
Consensus	(53)	IYLGSRASGVDPDRFGSGSGTDFTLKISRVEAEDVGVVYCMQ LQT					
Section 3							
	(105)	105	111				
CR2-1.49.1_LC	(105)	GTRLEIR		SEQ ID NO:45			
A19	(101)	-----		SEQ ID NO:8			
Consensus	(105)						





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**FIGURE 39**

**Figure 39A**

Section 1							
	(1)	1	10	20	30	40	51
CR2-1.51.1 HC	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSPTSYWIGWVRMPGKGLEWMGII					
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSPTSYWIGWVRMPGKGLEWMGII					
Consensus	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSPTSYWIGWVRMPGKGLEWMGII					
Section 2							
	(52)	52	60	70	80	90	102
CR2-1.51.1 HC	(52)	YPGDSDA YSPSFQGVITISADKSIISTAYLQWSSLKASDTAMYYCARHYDY					
VH5-51	(52)	YPGDSDT YSPSFQGVITISADKSIISTAYLQWSSLKASDTAMYYCAR----					
Consensus	(52)	YPGDSD KYSPSFQGVITISADKSIISTAYLQWSSLKASDTAMYYCAR					
Section 3							
	(103)	103	110	126			
CR2-1.51.1 HC	(103)	VWRNYRYTGWFDPWGQGLTVTVSS			SEQ ID NO:46		
VH5-51	(99)	-----			SEQ ID NO:6		
Consensus	(103)						

**Figure 39B**

Section 1									
	(1)	1	10	20	30	40	52		
CR2-1.51.1 LC	(1)	EIVLTQSPGTTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLITYGA							
A27	(1)	EIVLTQSPGTTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLITYGA							
Consensus	(1)	EIVLTQSPGTTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLITYGA							
Section 2									
	(53)	53	60	70	80	90	104		
CR2-1.51.1 LC	(53)	SNRATGIPDRFSGSGGTDTFTLTISRLEPEDFAVYYCQYGSLLPTFGPGTK							
A27	(53)	SNRATGIPDRFSGSGGTDTFTLTISRLEPEDFAVYYCQYGSLLPTFGPGTK							
Consensus	(53)	S R ATGIPDRFSGSGGTDTFTLTISRLEPEDFAVYYCQYGS							
Section 3									
	(105)	10508							
CR2-1.51.1 LC	(105)	VDIK	SEQ ID NO:47						
A27	(97)	----	SEQ ID NO:10						
Consensus	(105)								



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**FIGURE 40**

**Figure 40A**

								Section 1	
	(1)	1	10	20	30	40	52		
Cur2-6.4.1 hc	(1)	QVQLVQSGAEVRKPGASVVFVSCKASGYTFTSYDINWVRQATGQGLEWMGW							N
VH1-8	(1)	QVQLVQSGAEVRKPGASVVRVSCKASGYTFTSYDINWVRQATGQGLEWMGW							N
Consensus	(1)	QVQLVQSGAEVRKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGW							N
								Section 2	
	(53)	53	60	70	80	90	104		
Cur2-6.4.1 hc	(53)	PNSGNTDYAQRKPGGRVTMTRDTSISTAYMELSSLRSEDTA							YYCVRGPGYSY
VH1-8	(53)	PNSGNTGYAQRKPGGRVTMTRNTSISTAYMELSSLRSEDTA							YYCAR-----
Consensus	(53)	PNSGNT YAQRKPGGRVTMTR TSISTAYMELSSLRSEDTAIYYC							R
								Section 3	
	(105)	105	110	125					
Cur2-6.4.1 hc	(105)	NYDYVYGMVWVGQGTTVTVSS				SEQ ID NO:48			
VH1-8	(99)	-----				SEQ ID NO:1			
Consensus	(105)								

**Figure 40B**

								Section 1
	(1)	1	10	20	30	40	52	
Cur2-6.4.1 Lc	(1)	EIVLTQSPGTL <del>SLSPGERATL</del> SCRASQSVSSSYLAWYQQRPGQAPRLITY						T
A27	(1)	EIVLTQSPGTL <del>SLSPGERATL</del> SCRASQSVSSSYLAWYQQRPGQAPRLITY						SA
Consensus	(1)	EIVLTQSPGTL <del>SLSPGERATL</del> SCRASQSVSSSYLAWYQQRPGQAPRLITY						A
								Section 2
	(53)	53	60	70	80	90	104	
Cur2-6.4.1 Lc	(53)	SSRATGIPDRFSGSGSGTD <del>FTLTISRLEPED</del> FAVYYCQYGSSECSFGQGTK						
A27	(53)	SSRATGIPDRFSGSGSGTD <del>FTLTISRLEPED</del> FAVYYCQYGSSE-----						
Consensus	(53)	SSRATGIPDRFSGSGSGTD <del>FTLTISRLEPED</del> FAVYYCQYGSSE						
								Section 3
	(105)	105	108					
Cur2-6.4.1 Lc	(105)	LEIK		SEQ ID NO:49				
A27	(97)	----		SEQ ID NO:10				
Consensus	(105)							